Randy

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 09/598,982C
Source: IFW16
Date Processed by STIC: 8/10/05

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CRF Errors Edited by the STIC Systems Branch

Serial Number: 09/598,982C CRF Edit Date: 8/10/05
Edited by: AZ

____ Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

____ Corrected the SEQ ID NO. Sequence numbers edited were:

_____

____ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

_____

____ Deleted: ___ invalid beginning/end-of-file text ; ___ page numbers

____ Inserted mandatory headings/numeric identifiers, specifically:

_____

____ Moved responses to same line as heading/numeric identifier, specifically:

_____

/ Other: converted submitted file to a generated PatentIn sequence listing

_____

Revised 09/09/2003

RAW SEQUENCE LISTING DATE: 08/10/2005
PATENT APPLICATION: US/09/598,982C TIME: 10:50:00

Input Set : A:\34506104.ST25.txt
Output Set: N:\CRF4\08102005\I598982C.raw

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      3 <110> APPLICANT: Niles, Andrew
      4       Maffitt, Mark
      5       Haak-Frendscho, Mary
      7 <120> TITLE OF INVENTION: RECOMBINANT PROTEOLYTIC TRYPTASES, ACTIVE SITE MUTANTS
THEREOF,
      8       AND METHODS OF MAKING SAME
     10 <130> FILE REFERENCE: 34506.104
     12 <140> CURRENT APPLICATION NUMBER: 09/598,982C
     13 <141> CURRENT FILING DATE: 2000-06-21
     15 <150> PRIOR APPLICATION NUMBER: 09/079,970
     16 <151> PRIOR FILING DATE: 1998-04-15
     18 <160> NUMBER OF SEQ ID NOS: 52
     20 <170> SOFTWARE: PatentIn version 3.3
     22 <210> SEQ ID NO: 1
     23 <211> LENGTH: 735
     24 <212> TYPE: DNA
     25 <213> ORGANISM: Homo sapiens
     28 <220> FEATURE:
     29 <221> NAME/KEY: CDS
     30 <222> LOCATION: (1)..(735)
     32 <400> SEQUENCE: 1
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     35 1               5                  10                  15
     37 agc ctg aga gtc cac ggc cca tac tgg atg cac ttc tgc ggg ggc tcc       96
     38 Ser Leu Arg Val His Gly Pro Tyr Trp Met His Phe Cys Gly Gly Ser
     39             20                  25                  30
     41 ctc atc cac ccc cag tgg gtg ctg acc gca gcg cac tgc gtg gga ccg      144
     42 Leu Ile His Pro Gln Trp Val Leu Thr Ala Ala His Cys Val Gly Pro
     43         35                  40                  45
     45 gac gtc aag gat ctg gcc gcc ctc agg gtg caa ctg cgg gag cag cac      192
     46 Asp Val Lys Asp Leu Ala Ala Leu Arg Val Gln Leu Arg Glu Gln His
     47     50                  55                  60
     49 ctc tac tac cag gac cag ctg ctg ccg gtc agc agg atc atc gtg cac      240
     50 Leu Tyr Tyr Gln Asp Gln Leu Leu Pro Val Ser Arg Ile Ile Val His
     51 65                  70                  75                  80
     53 cca cag ttc tac acc gcc cag atc gga gcg gac atc gcc ctg ctg gag      288
     54 Pro Gln Phe Tyr Thr Ala Gln Ile Gly Ala Asp Ile Ala Leu Leu Glu
     55                 85                  90                  95
     57 ctg gag gag ccg gtg aac gtc tcc agc cac gtc cac acg gtc acc ctg      336
     58 Leu Glu Glu Pro Val Asn Val Ser Ser His Val His Thr Val Thr Leu
     59             100                 105                 110
     61 ccc cct gcc tca gag acc ttc ccc ccg ggg atg ccg tgc tgg gtc act      384
     62 Pro Pro Ala Ser Glu Thr Phe Pro Pro Gly Met Pro Cys Trp Val Thr
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ggc tgg ggc gat gtg gac aat gat gag cgc ctc cca ccg cca ttt cct  432
Gly Trp Gly Asp Val Asp Asn Asp Glu Arg Leu Pro Pro Pro Phe Pro
 130                 135                 140
ctg aag cag gtg aag gtc ccc ata atg gaa aac cac att tgt gac gca  480
Leu Lys Gln Val Lys Val Pro Ile Met Glu Asn His Ile Cys Asp Ala
145                 150                 155                 160
aaa tac cac ctt ggc gcc tac acg gga gac gac gtc cgc atc gtc cgt  528
Lys Tyr His Leu Gly Ala Tyr Thr Gly Asp Asp Val Arg Ile Val Arg
                165                 170                 175
gac gac atg ctg tgt gcc ggg aac acc cgg agg gac tca tgc cag ggc  576
Asp Asp Met Leu Cys Ala Gly Asn Thr Arg Arg Asp Ser Cys Gln Gly
            180                 185                 190
gac tcc gga ggg ccc ctg gtg tgc aag gtg aat ggc acc tgg ctg cag  624
Asp Ser Gly Gly Pro Leu Val Cys Lys Val Asn Gly Thr Trp Leu Gln
        195                 200                 205
gcg ggc gtg gtc agc tgg ggc gag ggc tgt gcc cag ccc aac cgg cct  672
Ala Gly Val Val Ser Trp Gly Glu Gly Cys Ala Gln Pro Asn Arg Pro
    210                 215                 220
ggc atc tac acc cgt gtc acc tac tac ttg gac tgg atc cac cac tat  720
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Val Pro Lys Lys Pro
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Ser Leu Arg Val His Gly Pro Tyr Trp Met His Phe Cys Gly Gly Ser
            20                  25                  30
Leu Ile His Pro Gln Trp Val Leu Thr Ala Ala His Cys Val Gly Pro
        35                  40                  45
Asp Val Lys Asp Leu Ala Ala Leu Arg Val Gln Leu Arg Glu Gln His
    50                  55                  60
Leu Tyr Tyr Gln Asp Gln Leu Leu Pro Val Ser Arg Ile Ile Val His
65                  70                  75                  80
Pro Gln Phe Tyr Thr Ala Gln Ile Gly Ala Asp Ile Ala Leu Leu Glu
                85                  90                  95
Leu Glu Glu Pro Val Asn Val Ser Ser His Val His Thr Val Thr Leu
            100                 105                 110
Pro Pro Ala Ser Glu Thr Phe Pro Pro Gly Met Pro Cys Trp Val Thr
        115                 120                 125
Gly Trp Gly Asp Val Asp Asn Asp Glu Arg Leu Pro Pro Pro Phe Pro
    130                 135                 140
Leu Lys Gln Val Lys Val Pro Ile Met Glu Asn His Ile Cys Asp Ala
```

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142 145                 150                 155                 160
145 Lys Tyr His Leu Gly Ala Tyr Thr Gly Asp Asp Val Arg Ile Val Arg
146                 165                 170                 175
149 Asp Asp Met Leu Cys Ala Gly Asn Thr Arg Arg Asp Ser Cys Gln Gly
150             180                 185                 190
153 Asp Ser Gly Gly Pro Leu Val Cys Lys Val Asn Gly Thr Trp Leu Gln
154         195                 200                 205
157 Ala Gly Val Val Ser Trp Gly Glu Gly Cys Ala Gln Pro Asn Arg Pro
158     210                 215                 220
161 Gly Ile Tyr Thr Arg Val Thr Tyr Tyr Leu Asp Trp Ile His His Tyr
162 225                 230                 235                 240
165 Val Pro Lys Lys Pro
166                 245
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172 <213> ORGANISM: Artificial Sequence
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175 <223> OTHER INFORMATION: PCR primer
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182 <211> LENGTH: 40
183 <212> TYPE: DNA
184 <213> ORGANISM: Artificial Sequence
186 <220> FEATURE:
187 <223> OTHER INFORMATION: PCR primer
189 <400> SEQUENCE: 4
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195 <212> TYPE: DNA
196 <213> ORGANISM: Homo sapiens
199 <220> FEATURE:
200 <221> NAME/KEY: CDS
201 <222> LOCATION: (7)..(753)
203 <400> SEQUENCE: 5
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206       1               5                   10
208 aag tgg ccc tgg cag gtg agc ctg aga gtc cac ggc cca tac tgg atg      96
209 Lys Trp Pro Trp Gln Val Ser Leu Arg Val His Gly Pro Tyr Trp Met
210 15                  20                  25                  30
212 cac ttc tgc ggg ggc tcc ctc atc cac ccc cag tgg gtg ctg acc gca     144
213 His Phe Cys Gly Gly Ser Leu Ile His Pro Gln Trp Val Leu Thr Ala
214                 35                  40                  45
216 gcg cac tgc gtg gga ccg gac gtc aag gat ctg gcc gcc ctc agg gtg     192
217 Ala His Cys Val Gly Pro Asp Val Lys Asp Leu Ala Ala Leu Arg Val
218             50                  55                  60
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220 caa ctg cgg gag cag cac ctc tac tac cag gac cag ctg ctg ccg gtc      240
221 Gln Leu Arg Glu Gln His Leu Tyr Tyr Gln Asp Gln Leu Leu Pro Val
222         65                  70                  75
224 agc agg atc atc gtg cac cca cag ttc tac acc gcc cag atc gga gcg      288
225 Ser Arg Ile Ile Val His Pro Gln Phe Tyr Thr Ala Gln Ile Gly Ala
226     80                  85                  90
228 gac atc gcc ctg ctg gag ctg gag gag ccg gtg aac gtc tcc agc cac      336
229 Asp Ile Ala Leu Leu Glu Leu Glu Glu Pro Val Asn Val Ser Ser His
230 95                  100                 105                 110
232 gtc cac acg gtc acc ctg ccc cct gcc tca gag acc ttc ccc ccg ggg      384
233 Val His Thr Val Thr Leu Pro Pro Ala Ser Glu Thr Phe Pro Pro Gly
234                 115                 120                 125
236 atg ccg tgc tgg gtc act ggc tgg ggc gat gtg gac aat gat gag cgc      432
237 Met Pro Cys Trp Val Thr Gly Trp Gly Asp Val Asp Asn Asp Glu Arg
238             130                 135                 140
240 ctc cca ccg cca ttt cct ctg aag cag gtg aag gtc ccc ata atg gaa      480
241 Leu Pro Pro Pro Phe Pro Leu Lys Gln Val Lys Val Pro Ile Met Glu
242         145                 150                 155
244 aac cac att tgt gac gca aaa tac cac ctt ggc gcc tac acg gga gac      528
245 Asn His Ile Cys Asp Ala Lys Tyr His Leu Gly Ala Tyr Thr Gly Asp
246     160                 165                 170
248 gac gtc cgc atc gtc cgt gac gac atg ctg tgt gcc ggg aac acc cgg      576
249 Asp Val Arg Ile Val Arg Asp Asp Met Leu Cys Ala Gly Asn Thr Arg
250 175                 180                 185                 190
252 agg gac tca tgc cag ggc gac tcc gga ggg ccc ctg gtg tgc aag gtg      624
253 Arg Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Lys Val
254                 195                 200                 205
256 aat ggc acc tgg ctg cag gcg ggc gtg gtc agc tgg ggc gag ggc tgt      672
257 Asn Gly Thr Trp Leu Gln Ala Gly Val Val Ser Trp Gly Glu Gly Cys
258             210                 215                 220
260 gcc cag ccc aac cgg cct ggc atc tac acc cgt gtc acc tac tac ttg      720
261 Ala Gln Pro Asn Arg Pro Gly Ile Tyr Thr Arg Val Thr Tyr Tyr Leu
262         225                 230                 235
264 gac tgg atc cac cac tat gtc ccc aaa aag ccg tgaagcggcc gccgtcgt      771
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266     240                 245
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270 <211> LENGTH: 249
271 <212> TYPE: PRT
272 <213> ORGANISM: Homo sapiens
274 <400> SEQUENCE: 6
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281             20                  25                  30
284 Cys Gly Gly Ser Leu Ile His Pro Gln Trp Val Leu Thr Ala Ala His
285         35                  40                  45
288 Cys Val Gly Pro Asp Val Lys Asp Leu Ala Ala Leu Arg Val Gln Leu
289     50                  55                  60
```

```
292 Arg Glu Gln His Leu Tyr Tyr Gln Asp Gln Leu Leu Pro Val Ser Arg
293 65                  70                  75                  80
296 Ile Ile Val His Pro Gln Phe Tyr Thr Ala Gln Ile Gly Ala Asp Ile
297                 85                  90                  95
300 Ala Leu Leu Glu Leu Glu Glu Pro Val Asn Val Ser Ser His Val His
301             100                 105                 110
304 Thr Val Thr Leu Pro Pro Ala Ser Glu Thr Phe Pro Pro Gly Met Pro
305         115                 120                 125
308 Cys Trp Val Thr Gly Trp Gly Asp Val Asp Asn Asp Glu Arg Leu Pro
309     130                 135                 140
312 Pro Pro Phe Pro Leu Lys Gln Val Lys Val Pro Ile Met Glu Asn His
313 145                 150                 155                 160
316 Ile Cys Asp Ala Lys Tyr His Leu Gly Ala Tyr Thr Gly Asp Asp Val
317                 165                 170                 175
320 Arg Ile Val Arg Asp Asp Met Leu Cys Ala Gly Asn Thr Arg Arg Asp
321             180                 185                 190
324 Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Lys Val Asn Gly
325         195                 200                 205
328 Thr Trp Leu Gln Ala Gly Val Val Ser Trp Gly Glu Gly Cys Ala Gln
329     210                 215                 220
332 Pro Asn Arg Pro Gly Ile Tyr Thr Arg Val Thr Tyr Tyr Leu Asp Trp
333 225                 230                 235                 240
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337                 245
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343 <213> ORGANISM: Artificial Sequence
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346 <223> OTHER INFORMATION: Mutagenesis oligonucleotide
348 <400> SEQUENCE: 7
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358 <220> FEATURE:
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365        1               5                   10
367 aag tgg ccc tgg cag gtg agc ctg aga gtc cac ggc cca tac tgg atg       96
368 Lys Trp Pro Trp Gln Val Ser Leu Arg Val His Gly Pro Tyr Trp Met
369 15                  20                  25                  30
371 cac ttc tgc ggg ggc tcc ctc atc cac ccc cag tgg gtg ctg acc gca      144
372 His Phe Cys Gly Gly Ser Leu Ile His Pro Gln Trp Val Leu Thr Ala
373                 35                  40                  45
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